

### **AMENDMENTS TO THE CLAIMS**

Please amend the claims as shown below. A complete listing of the claims, including their current status identifier, is set forth below.

1-103. (Cancelled)

104. (New) A method for determining the expression level of a target gene in a tissue sample obtained from a human subject, comprising:

- (a) providing a polynucleotide complementary to an intronic sequence of a target gene,
- (b) hybridizing the polynucleotide to intronic RNA or a nucleic acid produced therefrom to form a complex
- (c) quantitatively detecting the complex to produce expression data, and
- (d) determining the expression level of the target gene based on the expression data

105. (New) The method of claim 104, further comprising determining if the expression level correlates with a clinical outcome, thereby determining a likelihood of the clinical outcome for the human subject.

106. (New) The method of claim 104, wherein the tissue sample is a resected tumor specimen or a tumor biopsy.

107. (New) The method of claim 106, wherein the tissue sample is formalin-fixed paraffin-embedded tissue.

108. (New) The method of claim 106, wherein the tissue sample comprises breast cancer tissue.

109. (New) The method of claim 104 further comprising determining a normalized expression level of the target gene relative to the expression level of one or more reference genes in the tissue sample.

110. (New) The method of claim 104, wherein the polynucleotide is immobilized on a solid surface and the complex is quantitatively detected using an array.

111. (New) The method of claim 104, wherein the polynucleotide is a primer and the complex is quantitatively detected using quantitative PCR.

112. (New) The method of claim 104, wherein the target gene is a human gene.

113. (New) The method of claim 104, wherein the polynucleotide is an oligonucleotide.